	-5	4	AG	CTG	CGG	000	GGI	CIG	CCA	GCC	AG/	rccc	TTI	GG/	GA	AGAC	:000	ACT	ccc	TGTC	
1	ΑT	GGG	000	CCC	CIG	CAC	CCI	GCF	.COC	CCI	TIC	TCI	1001	GGI	GC/	AGGI	GAC	AGC	GCT	GGCT	60
	М	G	Р	R	С	T	L	Н	Р	L	S	L	L	V	Q	V	I	A	L	Α	
61	GC	GAC	rcr	GGC	OCA	GGG	CAG	GCI	GCC	TGC	CII	CCI	000	CTC	TG	AGCI	CCA	GCC	CCA	CGGC	1.20
	Α	T	L	Α	Q	G	R	L	Р	A	F	L	Р	C	Ε	L	Q	P	Н	G	
121	CI	GGTY	GAA	CIG	CAA	CTG	GCI	CTI	CCI	GA/	GTC	CGI	GCC	:CCZ	CT:	ICIC	GGC	GGC	AGC	CCC	180
	L	V	N	С	N	W	L	F	'n	K	S	V	P	Н	F	S	Α	A	Α	P	
181	Œ	GGO	CAAC	CGT	CAC	CAG	CCI	CTC	CTI	ACT	CIC	CAA	1000	CAT	CCZ	ACCA	CTI	GCA	CGA	CICT	240
	R	Α	N	V	Τ	S	L	Ş	L	L	S	N	R	Ι	Н	Н	L	Н	D	S	
241	GA	CTT	KI	CCA	CCT	GTO	CAG	CCI	ACC	AAC	TCI	CAA	CCI	CAA	GT(	GGAA	CTC	CCC	GCC	GGCT	300
	D	F	V	Н	L	S	S	L	R	T	ŭ	N	L	K	W	N	C	P	Р	Α	
301	GG	CCT	AG	000	CAT	GCA	CTI	CCC	CTG	CCA	CAI	GAC	CAT	CGA	GC(	CCAA	CAC	CIT	CCI	GGCC	360
	G	L	S	P	М	Н	F	Р	С	Н	M	T	Ι	Ε	P	N	T	F	L	Α	
361	GT	300(	ZAC	CCT	GGA	GGA	GCT	GAA	CCT	GAG	CTA	CAA	CAC	CAI	CA(	CGAC	CGI	GCC	TGC	OCTG	420
	V	P	Τ	L	Ē	E	L	N	L	S	Y	N	S	Ι	T	Τ	V	P	Α	L	
421	$\varpi$	OGA(	CIC	CT	CGI	GTO	CCI	GTC	GCT	GAG	000	CAC	CAA	CAI	CC.	IGGT	GCI	AGA	000	CACC	480
	Ρ	D	S	L	V	S	L	S	L	S	R	T	N	Ι	L	V	L	D	P	Τ	
481	CA	CTO	CAC	TGG	CCI	ACA	TGC	CCT	GCG	CTA	CCI	GTA	CAI	:GGA	TG	GCAA	CTG	CTA	CTA	CAAG	540
	Н	L	T	G	L	Н	Α	L	R	Y	L	Y	М	D	G	N	С	Y	Y	K	
541	ΑA	0000	CIG	CA	GGG	GGO	GCI	GGA	.GGT	GGI	ĠΩ	GGG	TGC	CCT	CC.	rcgg	CCI	GGG	CAA	CCTC	600
	N	Р	С	Q	G	A	L	Ε	V	V	Ρ	G	Α	L	L	G	L	G	N	L	
601	AC	ACA:	rct	CTC	ACT	CAA	GTA	CAA	CAA	TCT	CAC	GGA	GGT	'GCC	000	GCAG	CCI	GCC	000	CAGC	660
	T	Н	L	S	L	K	Y	N	N	L	Τ	E	V	P	R	S	L	P	P	S	
661	CT	GA(	JAC!	CT	GCT	GTT	GTC	CTA	CAA	CCA	CAI	TGT	CAC	CCI	GA(	CGCC	TGA	GGA	CCT	GGCC	720
	L	Ε	Τ	L	L	L	S	Y	N	Н	I	V	Τ	L	T	P	E	D	L	Α	
721	ΑA	ICT(	JAC'	ľGO	CCT	GCG	CGT	GCI	TGA	TGI	GGG	GGG	GAA	CTC	CC	300G				TGCC 1 1-8	780
	N	L	T	A	L	R	V	L	D	V	G	G	N	С	R	R	С	D	Н		

781	OG	CAA	000	CTG	CAC	GGA	GTO	30CC	'AAA	GGA	CCA	CCC	CAA	GCT	GCA	CTC	TGA	CAC	CTT	CAGC	840
	R	N	D	С	R	E.	C	р	K	D	Н	р	K	Ī.	Н	S	ח	Т	F	S	0.10
941	CA	cct	- GAG	aas	ייי מכוו	'CGA	AGC	ACT	GGT	TTT	··· YGAA	•	CAC	TT	TCI	•	CAA	icci	'GGA	agaa	900
011	Н.	7.				E			V			D.	S	S	L	Y	N	I.	n	A	
901		-	-	•	AGC	act TOOT	-	_		_		GCT	-		GAG	-		CTT	oct	CTAC	960
701	R	W	F	R	G	J,	D	R	I.	0	V	Į,	D.	T,	S	E.	N	F	Ι.	γ	700
961		otg	- Cat		-	.GAC	CAC		CTT	-	GG:		GG(	 :000:		'nΩ:	•	KGCT	CAA	-	1020
701	D	C	I	T	K	Т	T	А	F	0	G	L	A	R	T,	R	K	 [,	N	Γ.	2020
1021	TO	CTT	- Caa	- TTA	CCA	CAA	GAA	GGT	GTC	~	TGC		 .CCT	GCA	CCT	GGC	 'ACC	CIC	CTT	TGGG	1080
1001	S	F	N	Υ	Н	K	K	V	S	F	A	Н	L	Н	L	A	P	S	F	G	
1081	CA	- CCT	 COG	GTO	CCT	'GAA	GGA	GCT	'GGA	- CAT	GCA	TGG	CAT	CTI	CTT	000	- CTC	GCT	CAG	TGAG	1140
.001	Н	L	R	S	L	K	E	L	D	М	Н	G	I	F	F	R	S	L	S	Е	
1141	AC	- CAO	GCT	- CCA	ACC	TCI	GGT	CA	ACT	GCC	TAT	GCT	CCA	.GAC	CCI	GOG	CCI	GCA	GAT	GAAC	1200
	T	T	L	0	Р	L	V	0	L	Р	М	L	0	Т	L	R	L	0	М	N	
1201	TT	CAT	TAA	CCA	GGC	OCA	GCI	cag	CAI	CTT	TGG	GGC	CTI	'CCC	TGG	CCI	GCI	GTA	CGT	GGAC	1260
	F	I	N	Q	А	Q	L	S	Ι	F	G	Α	F	Р	G	L	L	Y	V	D	
1261	CT.	ATO	GGA	CAA	000	CAT	CAG	OGG	AGC	TGC	AAG	GCC	AGT	GGC	CAT	TAC	TAG	GGA	.GGT	GGAT	1320
	L	S	D	N	R	I	S	G	Α	A	R	P	V	Α	Ι	Τ	R	E	V	D	
1321	GG	TAG	GGA	GAG	GGT	CIG	GCI	GCC	TTC	CAG	GAA	CCT	ŒC	TOO	ACG	TCC	ACT	GGA	CAC	TCTC	1380
	G	R	Ε	R	V	W	L	Р	S	R	N	L	Α	Р	R	Р	, ,	D	T	L	
1381	09	CTC.	AGA	GGA	CTI	CAT	GCC	AAA	CTG	CAA	GGC	CTT	CAG	CTI	CAC	CTI	'GGA	CCI	GTC	TCGG	1440
	R	S	Ε	D	F	М	Р	N	С	K	Α	F	S	F	T	L	D	L	S	R	
1441	AA	CAA	CCT	GGT	GAC	AAT	CCA	GTC	GGA	GAT	GTT	TGC	TOG	CCI	CTC	ACG	CCI	CGA	GTG	CCTG	1500
	N	N	L	V	Τ	Ι	Q	S	Ε	М	F	A	R	L	S	R	L	Ξ	С	Ľ	
1501	Œ	TCT	GAG	CCA	CAA	CAG	CAI	CIC	CCA	GGC	GGT	CAA	TGC								1560
	R	Ĭ,	S	Н	N	S	T	S	0	Α	V	N	G	S (	o SE	ᇉ	Λ V O	D 10:	1 8 T.	ან-1 T	614)
	11	11	J	11	LV	J	1	U	~	rı.	•	TA		(	ŠĒ	QΊ	ďΝ	1Õ:	2 2	61-5	20)

1561 AGCCTCCGGGTGCTGGACCTGTCCCACAACAAGCTGGACCTGTATCACGGGGCGCTCGTTC 1620  S L R V L D L S H N K L D L Y H G R S F  1621 ACGGACCTGCCCCCCCTGGAAGCACTGGACCTCAGCTACAACAGCCAGC	_																					
1621 ACCACCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1561	AG	CCI	'GOG	GGI	GCI	GGA	CCT	GTC	CCP	CAA	CAA	GCT	GGA	CCI	GTA	ICA	CGG	GCG	CTC	GTTC	1620
TELPPRLEALD LSYNSQPFTM  1681 CAGGGGGGGGGGCCACACCTCAGCTTCGTGGCCCAGCTGCCCCGCCCTGCCCTCAGCTTACCTCAGC 1740  QGVGHNLSFVACACCCAGCTTCGTGGCCCAGCTGCCCGCCCTCACCTCA		S	L	R	V	L	D	L	S	Н	N	K	L	D	L	Y	Н	G	R	S	F	
1681 CAGGGTGTGGGCCACAACCTCAGCTTCGTGGCCCAGCTGCCCGCCC	1621	AC	GGA	GCT	GCC	GCC	CCT	GGA	AGC	ACT	GGA	CCI	CAG	CTA	CAA	CAG	CCA	GCC	CTT	TAC	CATG	1680
Q G V G H N L S F V A Q L P A L R Y L S  1741 CTGGGGGACAATGACATCCATAGGGGAGTGTGCCAGCAGGTCTGTAGGGCTCACTGTGC 1800  L A H N D I H S R V S Q Q L C S A S L C  1801 GCCTGGACTTTAGGGGGAGAGTGTGGGGGGAGTGTGGGGAGGACCTCTATCTC 1860  A L D F S G N D L S R M W A E G D L Y L  1861 CGCTTCTTCCAAGGGCTAGAGAACCACTGGACCTGGACCTGCCAGAACCACCTGCAC 1920  R F F Q G L R S L V W L D L S Q N H L H  1921 ACCCTCCTGCCAGGTGGCCCTGGACAACCTCCCCAAAAGCCTGAACCACTGCAC 1980  T L L P R A L D N L P K S L K H L H L R  1981 GACAATAACCTGGCCTTCTCAACTGGACCACCTCACCCTCCTGCCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCACCTGAAGGCCTCACCCTCCTGCCCAAGCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGGGGAGGTGGACCTCAGTGGCAACCTCGCCTTGTGAACCCTGGCTTCTT 2160  Q L R R L D L S G N S I G F V N P G F F  2221 CCCTCCTGGCCAAGCAGTTAGAAGCCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG  A L A K Q L E E L N L S A N A L K T V E  22221 CCCTCCTGGTTTGGCTGGATCGTGGGCAACCTCAACCTCAAGCTGGAGGCCCCAACCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCCCTCAAGCAGTGGAG  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGGCGCTGTGGGGGAGCCTTCGTGGGCCTTCTCTCTC		Τ	Ε	L	P	R	L	E	A	L	D	L	S	Y	N	S	Q	P	F	Τ	M	
1741 CTGGGGGACAATGACATCCATAGGGGAGTGTGCCAGGAGGCTCTGTAGGGGCTCACTGTGC 1800  L A H N D I H S R V S Q Q L C S A S L C  1801 GCCCTGGACTTTAGGGGGAGACTGAGGGGGAGTGTGGGGAGGAGCCTCTATCTC 1860  A L D F S G N D L S R M W A E G D L Y L  1861 CGCTTCTTCCAAGGGCTAGAGAACCACTGGACCTGGACCTGCCAGAACCACCTGCAC 1920  R F F Q G L R S L V W L D L S Q N H L H  1921 ACCCTCCTGCCAGGTGGCCCTGGACCACCTCCCCAAAAGCCTGAACCACTGCAC 1980  T L L P R A L D N L P K S L K H L H L R  1981 GACAATAACCTGGCCTTCTCAACTGGACCACCTCCCCCAAGCCTGCCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCACCTGAAGGCCTCACCCTCCTGCCCAAGCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGGGGGGGGGACCTCAGTGGCAACCTCGCCTAAGCTGGCACCTGCCCTTCTTT 2160  Q L R R L D L S G N S I G F V N P G F F  2221 CCCCTCTGGCCAAGCAGTTAGAGGCCCCAACCCTCAAGCCTGAAGCCCTCAAGCAGTGGAG  A L A K Q L E E L N L S A N A L K T V E  22221 CCCTCCTGGTTTGGCTGGATGGTGGGCAACCTGAAAGTCCTAGACGTGGAGGCCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGGCCCTGTGGGGGAGCCTTGTGGGCACCTTCTCTCTGTGGCACCTTCCGTTCCCTTTGTTTCTCTCTTTTTTTT	1681	CA	GGG	TGT	GGG	CCA	CAA	CCT	CAG	CTI	ŒI	GGC	CCP	GCI	GCC	CGC	CCT	GŒ	CTA	CCT	CAGC	1740
L A H N D I H S R V S Q Q L C S A S L C  1801 GOCCTGGACTTTAGGGGGAACGATCTGAGGCGGATGTGGGCTGAGGGAGACCTCTATCTC 1860 A L D F S G N D L S R M W A E G D L Y L  1861 CGCTTCTTCCAAGGGCTAAGAAGGCTTAGTCTGGCTGGACCTGTGCCAGAACCACCTGCAC 1920 R F F Q G L R S L V W L D L S Q N H L H  1921 ACCCTCCTGCCAAGGTGGCCTTGACAAGCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT : 980 T L L P R A L D N L P K S L K H L H L R  1981 GACAATAACCTGGCCTTCTCAACTGGAGCACCCTCACCCTCCTGCCCAAGCTGGAAACC 2040 D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCACCTGAAGGCCTGAAGCTGCCAAGCTGGCACC 2100 L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGGGGGGGGGGGCCTGAGGCACCTCAGCCTGGCTCTTT 2160 Q L R R L D L S G N S I G F V N P G F F  2161 CCCTGGCCAAGCAGTTAGAAGACCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG A L A K Q L E E L N L S A N A L K T V E  22221 CCCTCCTGGTTTGGCTGGGCAACCTCAACCTCAAGACGTGGAGGCCCAACCCT 2280 P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGGCCCTGTGGGGGAGACCTTGTGGGCACCTTCTGCGACCTTCCGTTG 2340 L H C A C G A T F V G F L L E V Q A A V		Q	G	V	G	Н	N	L	S	F	V	A	Q	L	P	A	L	R	Y	L	S	
1801 GOCTGGACTTTAGCGGCAACGATCTGAGCGGATGTGGGCTGAGGGAGACCTCTATCTC 1860  A L D F S G N D L S R M W A E G D L Y L  1861 CGCTTCTTCCAAGGGCTAAGAAGCCTAGTCTGGCTGGACCTGTGCCAGAACCACCTGCAC 1920  R F F Q G L R S L V W L D L S Q N H L H  1921 ACCCTCCTGCCAAGGTGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT : 980  T L L P R A L D N L P K S L K H L H L R  1981 GACAATAACCTGGCCTTCTCAACTGGACCACCCTCCCTGCCCAAGCTTGCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCACCTGAAGGCCTCAACCTCCTGCCCAAGCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGCGGAGGTGGACCTCAGTGGCAACCTCGGCTTTTT 2160  Q L R R L D L S G N S I G F V N P G F F  2161 CCCTGGCCAAGCAGTTAGAAGCCTCAACCTCACCGCCAATGCCCTCAAGACAGTGGAG  A L A K Q L E E L N L S A N A L K T V E  22221 CCCTCCTGGTTTGGCTGGACATCGTGGCCAACCTCAAGCCAGTGGAGCCCAACCTCAAGCACTTGGTTTT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCGCCTGTGGGGGAACCTTGTGGGCCTTCTCTGTGAACCCTTGCGTGCCTTCCTGTGGCACCTTGCTGCGCTTGCTGGCTTCCTGTGGACCTCCACCTTGTGGACCTCCACCCTGGACTTCACCCTCCAGCCCCAAGCCCTGAAGCCCTCAAGCCTTGAAGCTCAAGCCCTCCAAGCCCTCCACCCCCCAAGCCCCCCAAGCCCCCCAAGCCCCCCAAGCCCCCC	1741	CT	GGC	GCA	CAA	TGA	CAT	CCA	TAG		AGT	GTC	CCP	GCA	GCT	CIG	TAG	CGC	CTC	ACT	GTGC	1800
A L D F S G N D L S R M W A E G D L Y L  1861 CGCTTCTTCCAAGGCUTAAGAAGCCTAGTCTGGCTGGACCTGTCCCAGAACCACCTGCAC 1920  R F F Q G L R S L V W L D L S Q N H L H  1921 ACCCTCCTGCCAGTGCCCTGGACACCTCCCCAAAGCCTGAAGCATCTGCATCTCCGT 1980  T L L P R A L D N L P K S L K H L H L R  1981 GACAATAACCTGGCCTTCTCAACTGGACCACCTCCTGCCCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCACCTGAAGGCCTGACACCTCCCCAAGCTGGCATCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGCGGAGGCTGGACCTCAGTGCCAACAGCATCGGCTTTTT 2160  Q L R R L D L S G N S I G F V N P G F F  2161 GCCCTGCCCAAGCAGTTAGAAGACCTCAACCTCAGCCCCAATGCCCTCAAGACAGTGGAG  A L A K Q L E E L N L S A N A L K T V E  22221 CCCTCCTGGTTTGGCTGATCGTGGCCAACCTCAAAGTCCTAGAGCGTGGAGCCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCCCCTGTGGGGGAGACCTTGTGGGCTTCTCTCTC		L	Α	Н	N	D	Ι	Н	S	R	V	S	Q	Q	L	С	S	Α	S	L	С	
1861 COCTTCTTCCAAGGCUTAAGAAGCCTASTCTGGCTGGACCTGTCCCAGAACCACCTGCAC 1920 R F F Q G L R S L V W L D L S Q N H L H 1921 ACCCTCCTGCCAGTGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT 1980 T L L P R A L D N L P K S L K H L H L R 1981 GACAATAACCTGGCCTTCTCAACTGGACCACCCTCCTGCCCAAGCTGGAAACC 2040 D N N L A F F N W S S L T L L P K L E T 2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCTGAAGCAGCTGCCATCTGGCACC 2100 L D L A G N Q L K A L S N G S L P S G T 2101 CAGCTGGGGGGGACCTGAAGCACAGCATCGGCTTTTT 2160 Q L R R L D L S G N S I G F V N P G F F 2161 GCCCTGCCCAAGCAGTTAGAAGACCTCAACCTCAGCCCCAATGCCCTCAAGACAGTGGAG 2220 A L A K Q L E E L N L S A N A L K T V E 2221 CCCTCCTGGTTTGGCTGGATGGTGGGCAACCTCAAAGTCTAGACGTGAACCCT 2280 P S W F G S M V G N L K V L D V S A N P 2281 CTGCACTGCCCCTGTGGGGGAGACCTTGTGGGCTTCTCTCTGCTGGACCTTCAGTGACCTTGAAGCTTGAACCTTGCTGTTCAACCTTGCTGTTTCGACCCTTGTTGGACCCTTGAAGCTTGAAGTCCTAAGACAGTTGAAGCCTTCAAGACAGTTGAAGCACTTCAAGACAGTTGAAGCACTTCAAGACAGTTGAAGCACTTCAAGACAGTTGAAGCACTTCAAGACAGTTGAAGCACTTCAAGACAGTTGAAGCACTTCAAGACAGTTGAAGCACTTCAAGACAGTTGAAGACAGTTGAAGCACTTCAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACCTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACAGTTGAAGACCTTGAAGACCTTCAAGACCTTGAAGACTTCAAGACAGTTGCAGACAGCAGTTGCAGAGTACAGACTTGAAGACAGTTGAAGACCTTGAAGACCTTCAAGACCTTGAAGACCTTGAAGACCTTCAAGACCTTGAAGACACTTGAAGACCTTGAAGACCTTGAAGACCTTGAAGACCTTGAAGACACTTGAAGACCTTGAAGACCTTGAAGACCTTGAAGACCTTGAAGACACACAC	1801	GC	CCT	GGA	CTI	TAG	CGG	CAA	CGA	TCT	'GAG	CCC	GAI	GIG	GGC	TGA	GGG	AGA	CCT	CTA	TCTC	1860
R F F Q G L R S L V W L D L S Q N H L H  1921 ACCCICCTGCCACGTGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT :980  T L L P R A L D N L P K S L K H L H L R  1981 CACAATAACCTGGCCTTCTTCAACTGGACCACCCTCACCCCTGCCCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCTGCCATCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGCGGAGGCTGAACCTCAGTGCCAACAGCATCGGCTTTTTGTGAACCCTGGCTTCTTT 2160  Q L R R L D L S G N S I G F V N P G F F  2161 GCCCTGGCCAAGCAGTTAGAAGACCTCAACCTCAGCCCAATGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E  2221 CCCTCCTGGTTTGGCTGGTGGGCAACCTCAAGACCTCAAGACTGCAGCTGAAGCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCCCCTGTGGGCGAACCTTGTGGCCTTCTCTCTC		Α	L	D	F	S	G	N	D	L	S	R	М	W	A	Ε	G	D	L	Y	L	
1921 ACCTOCTGCCACGTGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT :980  T L L P R A L D N L P K S L K H L H L R 1981 GACAATAACCTGGCCTTCTAACTGGACCAGCCTGACCCTCGCCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T 2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAAGTGGCAGCTGCCATCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T 2101 CAGCTGCGGAGGCTGGACCTCAGTGCCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160  Q L R R L D L S G N S I G F V N P G F F 2161 GCCCTGGCCAAGCAGTTAGAAGACCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E 2221 CCCTCCTGGTTTGGCTGATGGTGGGCAACCTGAAAGTCCTAGAGCTGGAGCCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P 2281 CTGCACTGCGCCTGTGGGCGAACCTTGTGGGCTTCTCTGCTGCAGCTACAGCTGGTG 2340  L H C A C G A T F V G F L L E V Q A A V	1861	CG	CTT	CIT	CCA	AGG	CCT	AAG	AAG	CCI	AGI	CTG	GCI	GGA	CCT	GTC	CCA	GAA	CCA	CCT	GCAC	1920
T L L P R A L D N L P K S L K H L H L R  1981 GACAATAACCTGGCCTTCTTCAACTGGACCAGCCTGACCCTCCTGCCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGCGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160  Q L R R L D L S G N S I G F V N P G F F  2161 CCCCTGCCCAAGCAGCTTAAGAAGCCTCAACCTCACGCCAAGTGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E  2221 CCCTCCTGGTTTGGCTGGTGGGCAACCTGAAAGTCCTAGAGCTGGAGCCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCCCTGTGGGCGAACCTTGTGGGCTTCCTGCTGCAGCTGCAGCTGCGGTG 2340  (SCQ ID NO:1 1615-2394)  L H C A C G A T F V G F L L E V Q A A V		R	F	F	Q	G	L	R	S	L	V	W	L	D	L	S	Q	N	Н	L	Н	
1981 GACAATAACCTGGCCTTCTTCAACTGGACCAGCCTGACCCTGCCCAAGCTGGAAACC 2040  D N N L A F F N W S S L T L L P K L E T 2041 CTGGACTTGGCTGGAAACCAGCTGAAGGGCCTGAAGCATGGCAGCCTGCCATCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T 2101 CAGCTGGGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160  Q L R R L D L S G N S I G F V N P G F F 2161 GCCCTGGGCAAGCAGCATTAGAAGACCTCAACCTCAGCCCAATGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E 2221 CCCTCCTGGTTTGGCTGGATGGTGGGCAACCTCAAAGTCCTGAAGGTGAGCGCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P 2281 CTGCACTGGCGCTGTGGGGGGGCGACCTTGTGGGCTTCCTGCTGGGGGTTCCAGGCTGCGCTG 2340  (SCQ ID NO:1 1615-2394)  L H C A C G A T F V G F L L E V Q A A V	1921	AC	CCI	CCT	GCC	ACG	TGC	ÇÇT	GGA	CAA	$\alpha$	000	CAA	AAG	CCI	GAA	GCA	TCT	GCA	TCT	CCGT	1980
D N N L A F F N W S S L T L L P K L E T  2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T  2101 CAGCTGCGGAGGCTGGACCTCAGTGGCAACCAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160  Q L R R L D L S G N S I G F V N P G F F  2161 CCCCTGCCCAAGCAGTTAGAAGACCTCAACCTCAGCCCAATGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E  2221 CCCTCCTGGTTTGGCTGGATGGTGGGCAACCTCAAAGTCCTAGACGTGAGCGCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCGCCTGTGGGGGGAGACCTTGGTGGGCTTCCTGCTGGGAGTACAGCTGCGGTG 2340  (SCQ ID NO:1 1615-2394)  L H C A C G A T F V G F L L E V Q A A V		Τ	L	L	Р	R	A	L	D	N	L	P	K	S	L	K	Н	L	Н	L	R	
2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCACC 2100  L D L A G N Q L K A L S N G S L P S G T 2101 CAGCTGCGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160  Q L R R L D L S G N S I G F V N P G F F 2161 GCCCTGGCCAAGCAGTTAGAAGACCTCAACCTCAGCCCAATGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E 2221 CCCTCCTGGTTTGGCTCGATGGTGGGCAACCTCAAAGTCCTAGACGTGAAGCCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P 2281 CTGCACTGCGCCTGTGGGCGAACCTTGGTGGGCTTCCTGCTGGAGGTCACAGCTGCGCTG 2340  (SEQ ID NO:1 1615-2394)  L H C A C G A T F V G F L L E V Q A A V	1981	GΑ	CAA	TAA	CCI	GGC	CTT	CTT	CAA	CTG	GAC	CAC	CCI	GAC	CCI	ŒΤ	GCC	CAA	GCT	GGA	AACC	2040
L D L A G N Q L K A L S N G S L P S G T  2101 CACCTGOGGAGGCTGGACCTCAGTGGCAACCATCGCTTTGTGAACCCTGGCTTCTTT 2160 Q L R R L D L S G N S I G F V N P G F F  2161 COCCTGGCCAAGCAGTTAGAAGACCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG 2220 A L A K Q L E E L N L S A N A L K T V E  2221 COCTCCTGGTTTGGCTGGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGGCCCAACCCT 2280 P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCGCCTGTGGGGGGAGACCTTGGTGGGCTTCCTGCTGGAGGTACAGGCTGCGGTG 2340 (SEQ ID NO:1 1615-2394) L H C A C G A T F V G F L L E V Q A A V		D	N	N	L	A	F	F	N	M	S	S	L	T	$\Gamma$	L	P	K	L	Ε	T	
2101 CACCTGOGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160 Q L R R L D L S G N S I G F V N P G F F E 2161 COCCTGGCCAAGCAGTTAGAAGACCTCAACCTCAGGCCAATGCCCTCAAGACAGTGGAG 2220 A L A K Q L E E L N L S A N A L K T V E 2221 COCTCCTGGTTTGGCTGGATGGTGGGCAACCTGAAAGTCCTAGACGTGAAGTCAAGCCCAACCCT 2280 P S W F G S M V G N L K V L D V S A N P 2281 CTGCACTGCGCCTGTGGGGGGAGACCTTGGTGGGCTTCCTGCTGGAGGTACAGGCTGCCGTG 2340 (SEQ ID NO:1 1615-2394) L H C A C G A T F V G F L L E V Q A A V	2041	CT	GGA	CTT	GGC	TGG	AAA	CCA	GCT	'GAA	.GGC	CCI	'AAC	CAA	TGG	CAG	CCT	GCC	ATC	TGG	CACC	2100
Q L R R L D L S G N S I G F V N P G F F  2161 GCCCTGCCAAGCAGTTAGAAGACCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E  2221 CCCTCCTGGTTTGGCTGGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCGCCTGTGGGGGAGCCTTGGTGGGCTTCCTCCTGGAGGTACAGGCTGCCGTG 2340  (SEQ ID NO:1 1615-2394)  L H C A C G A T F V G F L L E V Q A A V		L	D	L	Α	G	N	Q	L	K	Α	L	S	N	G	S	L	Р	S	G	T	
2161 GOCCTGGCCAAGCAGTTAGAAGACCTCAACCTCAAGCCAATGCCCTCAAGACAGTGGAG 2220  A L A K Q L E E L N L S A N A L K T V E 2221 COCTOCTGGTTTGGCTGGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P 2281 CTGCACTGCGCCTGTGGGGGACCTTGGTGGGCTTCCTGGAGGTACAGCTGCCGTG 2340  (SEQ ID NO:1 1615-2394)  L H C A C G A T F V G F L L E V Q A A V	2101	CA	GCT	GOG	GAG	GCT	GGA	CCT	CAG	TGG	CAA	CAG	CAI	CGG	CTI	TGT	GAA	$\alpha$	TGG	CTT	CTTT	2160
A L A K Q L E E L N L S A N A L K T V E  2221 COCTOCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280  P S W F G S M V G N L K V L D V S A N P  2281 CTGCACTGCGCCTGTGGGGGACCTTGGTGGGCTTCCTGCTGGAGGTACAGGGTGCAGGTG 2340  (SEQ ID NO:1 1615-2394)  L H C A C G A T F V G F L L E V Q A A V		Q	L	R	R	L	D	L	S	G	N	S	I	G	F	V	N	P	G	F	F	
2221 COCTOCTGGTTTGGCTGGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280  PSWFGSMVGNLKVLDVSAAND 2281 CTGCACTGCGCCTGTGGGCGACCTTCGTGGGCTTCCTGCTGGAGGTACAGGCTGCCGTG 2340 (SEQ ID NO:1 1615-2394)  LHCACGATFVGFLLEVQAAV	2161	GC	CCI	GGC	CAA	.GCA	GTT	AGA	AGA	GCI	CAA	CCT	CAG	XCGC	CAA	TGC	CCT	CAA	GAC.	AGT	GGAG	2220
PSWFGSMVGNLKVLDVSANP 2281 CTGCACTGCGCCTGTGGGGCACCTTCGTGCGCCTTCCTGCTGCACGTACACGCTGCCGTG 2340 (SEQIDNO:1 1615-2394) LHCACGATFVGFLLEVQAAV		Α	L	Α	K	Q	L	Ε	Ε	L	N	L	S	Α	N	A	L	K	Τ	V	E	
2281 CTGCACTGCGCCTGTGGGGCACCTTCGTGGGCTTCCTGCTGCACGTACACGCTGCCGTG 2340 (SEQ ID NO:1 1615-2394) L H C A C G A T F V G F L L E V Q A A V	2221	CC	CTC	CIG	GTI	TGG	CTO	GAT	GGT	GGG	CAA	CCT	GAA	AGT	ŒΊ	AGA	CGT	GAG	CGC	CAA	CCCT	2280
(SEQID NO:1 1615-2394)		Р	S	W	F	G	S	М	V	G	N	L	K	V	L	D	V	S	Α	N	P	
LHCACGATFVGFLLEVQAAV	2281	ĈŢ	GCA	CTG	CGC	CTG	TGG	GGC	GAC	CT	VGT	GGG	CTI	CCI								
		,	ш	C	Λ	C	C.	Α	т	E	17	C	r	ī	- '		]] د ۱۲	N כ ∩	O:1	16 A	515-2 V	2394)
		ىد	Π	U	Μ	C	U	n	1	£	٧	G	Ľ	L			a <sup>v</sup> ic	йc	O:2	52	21-78	30)

2241	co	TV-C	COM	000	CAC	~~	CCT	C2.7	CTIC	TCC	רארי	TOT	222	777	CCT	יערטי		CCN	TAC	CATC	2400
2341	-						V											H		T	2400
0.404	Б	-	_	_	-							-		~		-		•••	~	~	2450
2401																					2460
	-		-	_			L											F			
2461	TO	GCT	GCT	GGQ	CAT	GGO	CCT	GGG	$\alpha$ 1	GGT	TGT	GOC	CAI	GCT	GCA	CCA	CCI	CTG	OGG	CTGG	2520
	S	L	L	Α	М	A	L	G	L	V	V	P	М	L	Н	H	Ţ	C	G	M	İ
2521	GA	CCT	CIG	GTA	CIG	CTT	CCA	CCT	GIG	$\alpha$ T	GGC	CTG	GCT	'GCC	CCA	CCG	AGG	GCA	GCG	GCGG	2580
	D	L	W	Y	С	F	Н	L	Ç	L	Α	W	L	P	Н	R	Ġ	Q	R	R	
2581	GG	OGC	AGA	OGO	CT	GIT	CTA	TGA	TGO	CTT	CGT	GGI	CII	TGA	CAA	AGC	TCA	GAG	TGC	TGTG	2640
	G	Α	D	Α	L	F	Y	D	Α	F	V	V	F	D	K	A	Q	S	Α	Λ	
2641	GO	OGA	CTG	GGT	GTA	CAA	CGA	GCT	GCG	GGT	GCA	GCI	GGA	.GGA	GCC	CCG	TGG	GCG	CCg	CGCA	2700
	Α	D	W	V	Y	N	Ε	L	R	V	0	L	E	E	R	R	G	Ŕ	R	A	
2701	CTN	300	CCT	GTG	CCT	GGA	GGA	GOG	AGA	CTG	- GTT	ACC	TGG	CAA	GAC	GCT	CTT	CGA	GAA	CCTG	2760
																		E			
2761		٠.		-	_	_	_					-									2820
2101							S												R		2020
2021			-		_	-	-			-		_			-				- `	•	2880
2021						-												D			2000
2001	-	-	_	_			-	-	_			~	~								2040
2881	.,																				2940
	_						-			•	-		_		-		-	V	•	_	
2941			-																		3000
		~					~								_			G	_		
3001	AG	CTT	CTG	GGC	CCA	GCT	GGG	CAC	AGC	IXI	GAC	CAG	GGA	CAA	.CCC	CCA	CTT	CTA	TAA	CCGG	3060
	~	F			*		G	-			-		_				-	-	•••	R	
3061	. AA	CTT	CTG	CCG	GGG	(CCC	CAC	GAC	AGC	)CG/	ATA	G	309	33 (8	SEC	) IC	N(	O:1	23	395-3	3147)
	N	F	С	R	G	Р	T	T	Α	Е	*			(5	SEC		N	<b>D:2</b>	78	31-10	30)

SWINE	1	${\tt MOPRCTLHPLSILLVQVIALAATLAQGRLPAFIPCELQPHGLVNCMLFIKSVPHFSAA}$	58	SWINE	
HUMAN	1	${\tt MCP-CRSALHPLSLLVQALIMLAMILALGTLPAFLPCELQPHGLVMCMMLFLKSVPHFSMA}$	59	HUMAN	
MOUSE	1	${\tt MARRET-LHPLSLLMQAAVLAETLALGTLPAFLPCELKPHGLMDCTWLFLKSVPRESAA}$	59	MOUSE	
CAT	1	MCP-CHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHESAA	59	CAT	
		* ******** ** ** ******** ** * *******			
SWINE	59	APRANYTSLSLLSNRIHHLHDSDEVHLSSLRTINLKWNCPPAGLSPMHEPCHMI IEPNIT	118	SWINE	
HUMAN	60	APROWISLSLSSNRIHHLHDSDFAHLPSLRHLNLKWCPPVGLSPMFFPCHMT1EPSTF	119	HUMAN	
MOUSE	60	ASCENITRISLIENRIHHIHNSDEVHILSNIRQINIKWNCPPTGLSPIHESCHMI'IEPRTF	119	MOUSE	
CAT	60	APRGIVITSLSLYSNRIHHLHDSDFVHLSSLRRINLKWICPPASLSPMFPCHMTIEPHIF	119	CAT	
		*,, *.*,*** ******** **,.** ******** ,***,** **			
SWINE	119	LAVPTLEEINLSYNSITTVPALPDSLVSLSLSRINILVLDPTHLTGLHALRYLYMDGVCY	178	SWINE	
HUMAN	120	LAVPTLEEINLSYNNIMIVPALPKSLISLSLSHINIIMLDSASLAGLHALRFIFMDQXCY	179	HUMAN	
MOUSE	120	LAMPITEELNLSYNGITTVPRLPSSLVNLSLSHINILVLDANSLAGLYSLRVLFMDQXCY	179	MOUSE	
CAT	120	LAVPTLFEIMLSYNSITTVPALPSSLVSLSLSRTNILVLDPAMLAGLHSLRFLFIDQXCY	179	CAT	
		**,,********* *,***,** **,.*** ****,** *,**, ** *,.****			
SWINE	179	YKNPCQCALEVVPCALLGLCNLTHLSLKYNNLTEVPRSLPPSLETLLLSYNHIVTLTPED	238	SWINE	
HUMAN	180	YKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPED	239	HUMAN	
MOUSE	180	YKNPCTGAVKVIPGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYLLVSYNLIVKLCPED	239	MOUSE	
CĄT	180	YMPCPQALQVAPGALLGLONLTHLSLKYNNLTAVPRGLPPSLEYLLLSYNHLITLAPED	239	CAT	
		***** * * * ****** ******** *** ** ** *			
SWINE	239			1-298)	
HUMAN	240			1-299)	
MOUSE	240	$ \begin{array}{c} {\tt LANLISLRVLD} {\tt MGGNCRRCD} {\tt HAPPPCIECGQKSLHLHPETFHLSHLEGIVIKDSSLHTL} \\ {\tt (SEQ~ID~NO} \end{array}$		1-299)	
CAT	240	LANLITALEVILDVSSICERCOHARNPOREORKGEPHLIPPUTESHLINLLGSLVILDSSLVNL		1-299)	

SWINE	299	DARWFRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRKLNLSENYHKKVSFAHLHLAPS 358
HUMAN	300	${\tt NASWFRGLANLRVIDLSENFLYKCITKIKAFQGLIQIRKINLSFNYQKRVSFAHLSIAPS~359}$
MOUSE	300	NSSWFQGLVNLSVIDLSENFLYESINHINAFQNLIRLRKLNLSFNYRKKVSFARLHLASS 359
CAT	300	NPRWEHALGWIMVIDLSENFLYDCITKTTAFYCLAQLRRINLSENYHKKVSFAHLHLAPS 359
		** * * * ********* * * *** * * * *
SWINE	359	FGHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLY 418
HUMAN	360	${\tt FGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRY~415}$
MOUSE	360	${\tt FWILVSLQEINM*GIFFRSLNKYTLPWLADLPKLHITHLQM*FINQAQLSIFGIFRALRF~419}$
CAT	360	${\tt FGSLLSLQQLDM+GIFFRSLSETTLRSLV+LPMLQSL+LQMNFINQAQLSIFGAFPGLRY~419}$
		* * * * * * ******* .** * ** * * *******
SWINE	419	$\verb VDLSDNRISGAARPVAITREVDGR-ERVWLPSRNLAPRPLDTIRSEDFMPNCKAFSFTLD 47 $
HUMAN	420	VDLSDNRISGASELTATMGEADGG-EKWILQPGDLAPAPVDTPSSEDFRPNCSTLNFTLD 478
MOUSE	420	$\verb volsdnrisgPstlseatpeeaddaeQeellsadphpaplstpasknfmdrcknfkftm  4799999999999999999999999999999999999$
CAT	420	VDLSDNRISGAMELAAATGEVDGG-ERVRLPSGDLALGPPGTPSSEGFMPGCKTINFTID 478
		***************************************
SWINE	478	LSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKIDLYHG 53' (SEQ ID NO:2 299-537
HUMAN	479	LSRNMIVTVQPEMFAQLSHLQCLRISHNCISQAVNGSQFLPLTGLQVLDLSRNKIDLYHE 538 (SEQ ID NO:4 300-538
MOUSE	480	LGRUNIVTIKPEMFVNLGRIQCISISHNSIAQAVNGSQFIPLITNIQVIDISHNKIDLYHN 533 (SEQ ID NO:6 300-539
CAT	479	LCRNNLVTIQPEMFARLSRLQCLLLCRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG 538
		********* *** ** ** ** ** ** ** ** ** *
		(3EQ ID 110.8 300-330)

SWINE	538	RSFTELPRLFALDLSYNSQPFTMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSA	597
HUMAN	539	HSFTELPRLEALDLSYNSQPFQMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCST	598
MOUSE	540	KSFSELPQLQALDLGMSQPFSIKGIGHNFSFVAHLMLHSLSLAHNDIHTRVSSHINSN	599
CAT	539	RSFTELPRLFALDISYNSQPFSMQGVGHNISFVAQLPALRYLSLAHNDIHSRVSQQLCSA	598
		**.***.*.*.*.****	
SWINE	598	SLCALDFSGNDLSRMAEGDLYLPFFQGLRSLVWLDLSQNHLHTLLPRALDNLPKSLKHL	557
HUMAN	599	SLRALDFSGVALGHWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVL	558
MOUSE	600	${\tt SVPFIDFSGNCNCRNMDEGGLYIHFFQGLSGLLKIDLSQNLHILRPQNLDNLPKSLKIL} \\$	559
CAT	599	SLRAIDFSGIALSRMAEGDLYLXFFRGIRSLVRIDILSQNRLHITLIPRITLDNLPKSLRLL	558
		*********.*** **.** * ***** **.*.* * .******	
SWINE	658	$\label{thm:laptows} \textbf{HLRDNNLAFFNWSSLTLLPKLETIDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNP}  \\$	717
HUMAN	659	RLRDNYLAFFKWWSIHFLPKLEVIDLAGVRLKALTNGSIPAGTRLRRIDVSCNSISFVAP	718
MOUSE	660	SLRDNYLSFFNWISLSFLPNLEVLDLAGVQLKALTNGTLPNGTLLQKLDVSSNSIVSVVP	719
CAT	659	RLRDNYLAFFNWSSLVLLPRLEALDLAGNOLKALSNGSIPNGTOLORLDLSSNSISFVAS	718
		**** * ** * ** ** ** ** ** ** ** ** **	
SWINE	718	$\tt GFFALAKQLFEINLSANALKTVEPSWFGSMVGNLKVLDVSANPLHCACGATFVGFTLEVQ \\$	777
HUMAN	719	$\tt CFFSKAKELREINLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFILEVQ \\$	778
MOUSE	720	$\hbox{AFFALAVEI} \textit{KEVNLSHNILKTVDRSWFGP} \hbox{IVMNLTVLDVRSNPLHCACC} \hbox{AAFVDLLLEVQ}  \\$	779
CAT	719	${\tt SFFALATRLIPELNLSANALKTVEPSWFGSLAGTIKVLDVTQNPLHCACGAAFVDFILLEVQ}  {\tt ``}$	778
		**,.* * *,***,*,*** **** * ,*** *******,*,,,*****	
SWINE	778	AAVPCLPSRVKOSEPOQLOGHSIFAODIRICIDETISMOCFGISLIAMAIGIJVVPMIHIL (SEQ ID NO:2 538-8	
HUMAN	779	AAVPGLPSTVKOGSPOOLOGLSIFAODLRICIDEALSWOCFALSLIAVALGIGVPMLHIL (SEQ ID NO:4 539-8	838 38)
MOUSE	780	TKVPGLANGVKCGSPGQLQCRSIFAQDLRLCIDEVLSMDCFGLSLIAVAVGAVVPILHHL (SEQ ID NO:6 540-8	
CAT	779	AAVPGIPGHVKCGSPOOLQCRSIFAQDIRLCIDEALSWOCFGLSLLIVALGLAVPMLHHL	338
		(SEQ ID NO:8 539-8	38)

SWINE	838 CGWDLWYCE'HLCLAWLPHRGQRRGADALFYDAFVVFDKAQSAVADWYNELRVQLFER	895
HUMAN	839 CGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWYYNELRGQLEEC	898
MOUSE	$840~{\tt CSWDVWYCFHLCLAWLPLLARSRRSAQA-LPYDAFVVFDKAQSAVADWVYNELRVRLEGR}$	898
CAT	839 CONDLWYCFHLCLAWLPRRGRRRGAD-ALPYDAFVVFDKAQSAVADWVYNEIRVRLEER	896
	****, *********************************	
SWINE	$896\ {\tt RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQQRL}$	955
HUMAN	$899 \ {\tt RGRWALRICLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFILLAQQRL}$	958
MOUSE	899 RGRRALRICLEDRDWLPGQITLFENLWAS IYGSRKTIFVLAHTDRVSGIIRTSFILAQQRL	958
CAT	$897 {\tt RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHIDRVSGLLRASFILLaQQRL}$	956
	*** ****** ***** ****** * *** * *** ****	
SWINE	$956 \ LEDRKDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNR$	1015
HUMAN	959 LEDRKOVVVLVILSPDCRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGVALTRINH	1018
MOUSE	959 LEDRKOVVVLVILIRPDAHRSRYVRLRQRLCRQSVLFWPQQPNGQGGFWAQLSTALTRONR	1018
CAT	957 LEDRKOVVVLVILRPDAHRSRYVRLRØRLCRØSVLLWPHØPSGØRSFWAQLGTALTRDNØ	1016
	**************** ** ***************** ** ** ** ****	
SWINE	1016 HFYNRNFCRCPTTAE (SEQ ID NO:2 838-1030)	1030
HUMAN	1019 HFYNRNFCQQP-TAE (SEQ ID NO:4 839-1032)	1032
	,	1032
CAT	1017 HYNONFOROPITAE (SEQ ID NO:8 839-1031)	1031
	**** *** ** ***	